

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1-20 (canceled).

21. (Previously amended) A method for cleavage of a double-stranded DNA molecule characterized by a distorted structure, wherein said distorted structure results from ultraviolet radiation damage, a photoproduct, an abasic site, mismatched nucleotide pairing, a platinum diadduct, an intercalated molecule, an insertion deletion loop of five or fewer nucleotides or alkylation of a nucleotide or a uracil residue resulting from deamination of a cytosine residue, said method comprising the step of contacting a DNA molecule characterized by a distorted structure with a broadly specific DNA damage endonuclease selected from the group of endonucleases consisting of a stable truncated Uve1p identified by the amino acid sequence given in SEQ ID NO:4, wherein said Uve1p is at least 90% pure, and a fusion protein comprising a stable truncated Uve1p and a heterologous sequence, wherein said fusion protein is identified by the amino acid sequence given in SEQ ID NO:6.
22. (Previously entered) The method of claim 21, wherein said truncated Uve1p wherein said Uve1p is at least 90% pure and has the amino acid sequence as given in SEQ ID NO:4.
23. (Previously amended) The method of claim 21, wherein said fusion protein consists of the amino acid sequence given in SEQ ID NO:6.

24. (Previously entered) The method of claim 21 wherein the insertion deletion loop is of four or fewer nucleotides.
25. (Previously amended) A method for cleavage of a double-stranded DNA molecule characterized by a distorted structure, wherein said distorted structure results from an abasic site, mismatched nucleotide pairing, a platinum diadduct, an insertion deletion loop, alkylation of a nucleotide, the presence of a uracil residue resulting from deamination of a cytosine residue, said method comprising the step of contacting a DNA molecule characterized by a distorted structure with a broadly specific DNA damage endonuclease comprising an amino acid sequence selected from the group consisting of SEQ ID NO:36; SEQ ID NO:37; SEQ ID NO:38; and SEQ ID NO:39, under conditions allowing for enzymatic activity of said endonuclease, with the proviso that when the endonuclease comprises the amino acid sequence of SEQ ID NO:38, the distorted structure does not result from mismatched nucleotides.